

OX	NCBI_TaxID=6968;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Midgut;
RX	MEDLINE=97053012; PubMed=8897641

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RESULT 4
SMS1_MYOSC          STANDARD:      PRT:      14 AA.
ID   SMS1_MYOSC          ID   SMS1_MYOSC          ID   SMS1_MYOSC          ID   SMS1_MYOSC
AC   P20750;             AC   P20750;             AC   P20750;             AC   P20750;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Somatostatin I.
OS   Myoxocephalus scorpius (Shortorn sculpin) (baddy sculpin),
OS   Oncochynchus kisutch (Coho salmon), and
OS   Anguilla anguilla (European freshwater eel).
RA   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorphi; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC   Cottolidae; Cottidae; Myoxocephalus.
CX   NCBI_TaxId=8097, 8019, 7936;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=M.scorpius; TISSUE=Pancreas;
RC   MEDLINE=88029486; PubMed=2889597;
RA   Conlon J.M., Davis M.S., Falkner S., Thim L.;
RT   "Structural characterization of peptides derived from
RT   prosomatostatin I and II isolated from the pancreatic islets of two
RT   species of teleostean fish: the daddy sculpin and the flounder."
RL   Eur. J. Biochem. 168:647-652(1987).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=O.kisutch; TISSUE=Pancreas;
RC   MEDLINE=87055212; PubMed=2877919;
RA   Klimeskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
RA   Plimmet J.R., Andrews P.C., Gorman A.;
RT   "Characterization of coho salmon (Oncorhynchus kisutch). islet
RT   somatostatins ";
RL   Gen. Comp. Endocrinol. 63:252-263(1986).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=A.anguilla; TISSUE=Pancreas;
RC   MEDLINE=89065329; PubMed=2904391;
RA   Conlon J.M., Deacon C.F., Hazen N., Henderson I.W., Thim L.;
RT   "Somatostatin-related and glucagon-related peptides with unusual
RT   structural features from the European eel (Anguilla anguilla).";
RL   Gen. Comp. Endocrinol. 72:181-189(1988).
CC   -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOPROPIN.
CC   -1- SUBCELLULAR LOCATION: Secreted.
CC   -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
DR   PIR: S00172; S00172.
DR   PIR: B60842; B60842.
DR   PIR: A60840; A60840.
DR   InterPro: IPR004250; Somatostatin.
DR   Pfam: PF03002; Somatostatin_1.
RW   Hormone; Multigene family.
FT   DISULFID 3 14
SQ   SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match          32.8%; Score 21; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGORNF 11
      11 : 11
Db      1 AGCKNF 6

RESULT 5
SMS_ALIMI          STANDARD:      PRT:      14 AA.
ID   SMS_ALIMI          ID   SMS_ALIMI          ID   SMS_ALIMI          ID   SMS_ALIMI
AC   P31885;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Somatostatin-14.

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OS Alligator mississippiensis (American alligator), and
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxId=8496, 34903;
 RN [1]
 RP SEQUENCE.

RC SPECIES=mississippiensis; TISSUE=Stomach;
 RA MEDLINE=93324451; PubMed=8101369;
 RX Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 RN [2]
 RP SEQUENCE.

RC SPECIES=T.scripta;
 RX MEDLINE=90341082; PubMed=1974347;
 RA Conlon J.M., Hicks J.W.;
 RT "Isolation and structural characterization of insulin, glucagon and
 RT somatostatin from the turtle, Pseudemys scripta.";
 RL Peptides 11:461-466(1990).
 CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 DR PIR: C60414; C60414.
 DR InterPro: IPR004250; Somatostatin.
 DR Pfam: PF03002; Somatostatin; 1.
 KW Hormone.
 FT DISULFID
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CMC64;

Query Match 32.8%; Score 21; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 5.4e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGORNF 11
 Db 1 AGCKNF 6

RESULT 6
 ID TKL1_LOCM1 STANDARD; PRT; 9 AA.
 AC P16223;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustachykinin I (TK-1).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridoidea; Acrididae; Acridinae; Locusta.
 OX NCBI_TaxId=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=90184489; PubMed=2311766;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Locustachykinin I and II, two novel insect neuropeptides with
 RT homology to peptides of the vertebrate tachykinin family.";
 RL FEBS Lett. 261:397-401(1990).
 CC -1- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC OVIDUCT AND FOREGUT.
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 DR PIR: S08265; ECLQIM.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match 31.2%; Score 20; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 POGIACOR 9
 Db 2 POGFYVVR 9

RESULT 7
 ID MDH_ACIDE STANDARD; PRT; 17 AA.
 AC P80540;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
 GN MDH.
 OS Acidovorax delafieldii.
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
 OC Acidovorax.
 OX NCBI_TaxId=47920;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CCUG 12929;
 RX MEDLINE=97334132; PubMed=9190829;
 RA Charnock C.;
 RT "Structural studies of malate dehydrogenases (MDHs): MDHs in
 RT Brevundimonas species are the first reported MDHs in Proteobacteria
 RT which resemble lactate dehydrogenases in primary structure.";
 RL J. Bacteriol. 179:4066-4070(1997).
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) -> oxaloacetate + NADH.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 DR InterPro: IPR001252; Mdh.
 DR PROSITE: PS00068; MDH; PARTIAL.
 DR Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1662 MW; 110E811A516909E CRC64;

Query Match 31.2%; Score 20; DB 1; Length 17;
 Best Local Similarity 80.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GIAGQ 8
 Db 11 GAAGQ 15

RESULT 8
 ID FARD_CALVO STANDARD; PRT; 9 AA.
 AC P41868;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Calliphoridae 13.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
 OX NCBI_TaxId=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliphorin) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FAMRAMEIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR: D44787; D44787.
 DR Neuropeptide; Amidation.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1028 MW; 22D10693C87AB6D8 CRC64;

Query Match 29.7%; Score 19; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 AGORNF 11
 1111
 DB 1 AGODGF 6

RESULT 9
 PPCK_FASHE STANDARD; PRT; 10 AA.
 ID PPCK_FASHE
 AC P80525;
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative phosphoenolpyruvate carboxylase [GTP] (EC 4.1.1.32)
 DE (Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile protein 1) (Fragment).
 OS Fasciola hepatica (liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.
 OX NCBI_TaxID=6192;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95366993; PubMed=7639732;
 RA Tkalecic J., Ashman K., Meusen E.;
 RT Fasciola hepatica: rapid identification of newly excysted juvenile proteins.
 RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
 CC -1 CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate + CO(2).
 CC -1 SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] FAMILY.
 CC DR Interpro: IPR000364; PEP-carboxykin.
 CC DR PROSITE: PS00505; PEPCK-GTP; PARTIAL.
 KW Lyase; Decarboxylase; GTP-binding.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1069 MW; 8393A6187AA9C87A CRC64;

Query Match 29.7%; Score 19; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 9.2e+02;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 POGIAG 8
 1111
 DB 2 PDGFDE 8

RESULT 10
 UN37_CLOPA STANDARD; PRT; 14 AA.
 ID UN37_CLOPA
 AC P81358;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 37 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=M5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flensburg R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -1 MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.8, ITS MW IS: 44.7 kDa.
 FT NON_TER 14

SQ SEQUENCE 14 AA; 1579 MW; 05384662DEF99210 CRC64;

Query Match 29.7%; Score 19; DB 1; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 OGAG 7
 1111
 DB 10 OGKVG 14

RESULT 11
 C1QA_RAT STANDARD; PRT; 15 AA.
 ID C1QA_RAT
 AC P31720;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Complement C1q subcomponent, A chain (fragment).
 GN C1QA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93218657; PubMed=8464426;
 RA Wing M.G., Sellly D.J., Bridgman D.J., Harrison R.A.;
 RT "Rapid isolation and biochemical characterization of rat C1 and C1q.";
 RL Mol. Immunol. 30:433-440(1993).
 CC -1 FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT C1R(2)C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
 CC -1 SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. THE C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAIN. IN ADDITION TO THE MAJOR A:B AND C:C DIMER BANDS, RAT, UNLIKE HUMAN C1Q, CONTAINED MINOR DIMER SPECIES.
 CC -1 SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
 CC DR Interpro: IPR001073; C1q.
 CC DR PROSITE: PS01113; C1Q; PARTIAL.
 KW Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen; Repeat.
 FT DISULFID 4
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1488 MW; 1B3D8000B7793965 CRC64;

Query Match 29.7%; Score 19; DB 1; Length 15;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 GIAG 7
 1111
 DB 12 GVAG 15

RESULT 12
 FLAM_AZOCH STANDARD; PRT; 17 AA.
 ID FLAM_AZOCH
 AC P23002;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Flavodoxin A (FLDA) (Fragment).
 OS Azotobacter chroococcum mcd 1.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Azotobacter.
 OX NCBI_TaxID=355;
 RN [1]

RC STRAIN-MCD 1155; PubMed=1859358;
 RA MEDLINE=91315397; PubMed=1859358;
 RA Bapty S., Barker P.D., Hill H.A.O., Sanghera G.S., Dunbar B.,
 RA Ashby G.A., Eady R.R., Thorneley R.N.F.;
 RT "Direct electrochemistry of two genetically distinct flavodoxins
 RT isolated from *Asotobacter chroococcum* grown under nitrogen-fixing
 RT conditions.";
 RL Biochem. J. 277:313-319(1991).
 CC -1- FUNCTION: LOW-POTENTIAL ELECTRON DONOR TO A NUMBER OF REDOX
 CC ENZYMES.
 CC -1- COFACTOR: FMN.
 CC -1- SIMILARITY: BELONGS TO THE FLAVODOXIN FAMILY.
 DR InterPro: IPR001226; Flavodoxin.
 DR PROSITE: PS00201; FLAVODOXIN; PARTIAL.
 KW Electron transport; Flavoprotein; FMN.
 FT NON_TER 17
 FT THIOLEST 17
 SQ SEQUENCE 17 AA; 1692 MW; DE7B6DA36B24C7 CRC64;

Query Match 29.7%; Score 19; DB 1; Length 17;
 Best Local Similarity 37.5%; Pred. No. 1.6e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 SPOGIACO 8
 Db 9 SSSCVTKR 16

RESULT 13
 A2M_OCTVU STANDARD; PRT; 18 AA.
 ID A2M_OCTVU
 AC P30800;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2-macroglobulin homolog (Alpha-2-M) (fragment).
 OS Octopus vulgaris (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
 OC Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=6645;
 RN [1]
 RP SEQUENCE:
 RA MEDLINE=92344633; PubMed=1379044;
 RA Thøgersen I.B., Salvesen G., Brucato F.H., Pizzo S.V., Englund J.J.;
 RT "Purification and characterization of an alpha-macroglobulin
 RT proteinase inhibitor from the mollusc *Octopus vulgaris*.";
 RL Biochem. J. 285:521-527(1992).

CC -1- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A
 CC UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDYL SPLITTER,
 CC CALLED THE "BAIT REGION" WHICH CONTAINS SPECIFIC CLEAVAGE SITES
 CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT
 CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH
 CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST
 CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR
 CC WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE
 CC BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE
 CC COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.
 CC -1- SUBUNIT: MONOMER. DISULFIDE-LINKED.
 CC -1- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
 CC PIR: S23971; S23971.
 DR InterPro: IPR001599; MacroglobulinA2.
 DR Pfam: PF00207; A2M; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 KW Serine protease inhibitor; Glycoprotein; Plasma; Bait region.
 FT NON_TER 1
 FT THIOLEST 1
 FT NON_TER 5
 FT THIOLEST 8
 SQ SEQUENCE 18 AA; 2011 MW; D8D61C473D901C9D CRC64;

Query Match 29.7%; Score 19; DB 1; Length 18;
 Best Local Similarity 36.4%; Pred. No. 1.7e+03;

Matches 4; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 OY 2 PQGIAGORNFN 12
 Db 2 PSCGGEQNMN 12

RESULT 14
 OXYT_RAACL STANDARD; PRT; 9 AA.
 ID OXYT_RAACL
 AC P42994;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Glutitocin.
 OS Raja clavata (Thornback ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalea; Hymnosqualea; Pristiogaster; Batoidae;
 OC Rajiformes; Rajidae; Raja.
 OX NCBI_TaxID=7781;
 RN [1]
 RP SEQUENCE:
 RA MEDLINE=66123415; PubMed=5880565;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Phylogeny of neurohypophyseal peptides: Isolation of a new hormone,
 RT glutitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
 RT the ray (*Raja clavata*)."
 RL Biochim. Biophys. Acta 107:393-396(1965).
 CC -1- FUNCTION: ANTIDIURETIC HORMONE.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro: IPR000981; Neurohyp-horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DSUFLEID 1
 FT MOD_RES 9
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 984 MW; 17E9C76B455B04B CRC64;

Query Match 28.1%; Score 18; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PQG 4
 Db 7 PQG 9

RESULT 15
 CEPL_ACHFU STANDARD; PRT; 11 AA.
 ID CEPL_ACHFU
 AC P22790;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Cardio-excitatory peptide-1 (ACEP-1).
 OS Achatina fulica (Giant African snail).
 OC Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE:
 RA STRAIN-Ferussac; Tissue=Heart atrium;
 RA MEDLINE=90211261; PubMed=2322251;
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
 RT "A novel cardio-excitatory peptide isolated from the atria of the
 RT African giant snail, *Achatina fulica*.";
 RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
 CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
 CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
 CC MOVEMENT OF ACHATINA.
 CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLISIA.

Query Match 28.1%; Score 18; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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KW Hormone; Amidation. 11 AMIDATION.
FT MOD RES 11
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C741365 CRC64;

Query Match 28.18; Score 18; DB 1; Length 11;
Best local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 POG 4
111
Db 7 POG 9

Search completed: May 16, 2003, 10:37:29
Job time : 12 secs